



(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 530 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AAACATAAGT CCAGTTATCT ACAGGTACAG GTTGATGAGA GGCCTCTCCA TTTCCACCAC 60  
CTGCCTGTTG AGTGTCTCTC AGGCCATCAA CCTCACCCCA AGGAGCTCCC GTTTGGCAAT 120  
G TTCAGAGAT CCTCACATCA CAAACCGCGT TGCTTTCTCT TGCTGTGGGT CTTCCACATA 180  
TCCATTAGTG GAAGCTTCTT AGTCTCCACT CTTCCCTCCA AAAATGTTGC CTCAAATAGT 240  
GTTACATTTG TCACTCAATC CTGCTCTGCT GGGCCCCTGA GTTGCTTCCT TGGGCAGACA 300  
ATTTTCACAC TGATGACATT TCAGGATGTC TCCTTGCAGC TCATGGCCCC CTTCA GTGGA 360  
TACATGGTGA TTCTCTTG TG CAGGCATAAC AGGCAGTCTC AGCATCTTCA TAGTATCAAC 420  
CTTTCTCCAA AAGCACCCCC AGATAAAAGG GCCATCCAGA GCATTCTTTT GCTCGTGAGT 480  
TTCTTTGTGT TCATGTGCCT TTTCCATTT GCTGCCTTAA CACTTCTGTC 530

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1385 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

056943 090400 974550

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TTTCGGCACG AGTTCACCTG CCCTCGAATT TCAATTTGAG TAAGTGACCA GCAATGGAGT 60  
ACAGAATCAG AAGATGGTTG GATCCCAGGC AGGCTGTGGG AGGAGGAACT CTGGAACTGC 120  
ATGAGGAGTT TGAGCACCTG CCATGGAGTA GCTGATCTCT GAGGACCCCT CACACAGGTC 180  
CTGTGTTCTA CATCAAGTGC ATATTTTTTC TAGGATATTC ATTTCCGTAA GTCCTGAAAT 240  
TACTTAATTT TTATAGGAGT TCTCATATAT GATGAATAAG AACAGCAGAC TCTACACTGA 300  
TTCTAACATA AGGAATACCT TTTTCGCTGA AATTGGCATT GGAGTCTCAG CCAATAGCCT 360  
CCTACTTCTC TTCAACATCT TCAAGTTAAT TTGTGGGCAG AGGTCCAGAC TCACTGACCT 420  
GCCCATTGGT CTCTTGTCCT TAATCAACTT ACTTATGCTA CTGATGACGG CATTTCATAGC 480  
CACAGACACT TTTATTTCTT GGAGAGGGTG GGATGACATC ATATGTAAAT CCCTTCTCTA 540  
CCTGTACAGA ACTTTTAGAG GTCTCTCTCT TTGTACCAGC TGCCTGTTGA GTGTCCTGCA 600  
GGCCATCATC CTCAGTCCCA GAAGCTCCTG TTTAGCAAAG TTCAAACATA AGCCTTCCCA 660  
TCACATCTCC TGTGCCATTC TTTCTCTGAG TGTCTCTAC ATGTTCAATTA GCAGTCACCT 720  
CTTAGTATCC ATCATTGCCA CCCCAAATTT GACCACGAAT GACTTTATTC ATGTTACTCA 780  
GTGGTGCTCT ATTCTACCCA TGAGTTACCT CATGCAAAGC ATGTTTTCTA CACTGCTGGC 840  
CATCAGGGAT GTCTTTCTTA TTAGTCTCAT GGTCTGTCA ACATGGTACA TGGTGGCTCT 900  
CTTGTGTAGG CACAGGAAAC AGACCCGGCA TCTTCAGGGT ACCAGCCTTT CCCCCAAAGC 960  
ATCCCCAGAA CAAAGGGCCA CCCGTTCCAT CCTGATGCTC ATGAGCTTAT TTGTTCTGAT 1020

099846 0304  
106020 9486250

(2) INFORMATION FOR SEQ ID NO:3:

(A) LENGTH: 1331 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GTGGATCCCC	CGGGCTGCAG	GAATTCGGCA	CGAGCCGTGA	TTAAGGGACT	TTGAACTTTT	60
CAAGGGATTT	GGAGTTTTAT	GAAGAATTTG	AAGATTTACA	GAGTTTACAG	GAATGGAGCT	120
GACCAGCCAC	TATGACATGC	CTTATATCTC	CAAGAGCATA	AATATAAGGC	ATGGCATGAG	180
AGGACCAGCA	GCCACTGTTC	TCATATATGA	TGAATAAGAA	CAGCAGAGTC	CACACTGATT	240
CTACCATAAG	GAATACCTTC	TCCACTGAAA	TTGGCATTGG	AATCTTAGCC	AACAGTTTCC	300
TACTTCTCTT	CCACATCTTC	AAGTTTATTC	GTGGACAGAG	GTCCAGACTC	ACTGACCTGC	360

CCATTGGTCT CTTGTCCCTA ATCCACCTAC TGATGCTACT GATGGGGGCA TTCATAGCCA	420
TAGACATTTT TATTTCTTGG AGGGGATGGG ATGACATCAT ATGTAAATTC CTTGTCTACT	480
TGTACAGAAG TTTTAGAGGT CTCTCTCTTT GTACCACCTG CATGTTGAGT GTCCTGCAGG	540
CCATCACCTT CAGCCCCAGA AGCTCCTGTT TAGCAAAGTT CAAACATAAG TCTCCCCATC	600
ACGTCTCCTG TGCCATTATT TCGCTGAGCA TCCTCTACAT GTTCATTAGC AGTCACCTCT	660
TAGTATCCAT CAATGCCACC CCCAATTGA CCACGAACAA CTTTATGCAA GTTACTCAGT	720
CCTGCTACAT TATACCCTTG AGTTACCTCA TGCAAAGCAT GTTTTCTACA CTTCTGGCCA	780
TCAGAGATAT CTCTCTTATT AGTCTCATGG TCCTCTCGAC TTGTTACATG GAGGTTCTCT	840
TGTGTAGGCA CAGGAATCAG ATCCAGCATC TTCAAGGGAC CAACCTTTCC CCAAAGCAT	900
CTCCAGAACA AAGGGCCACA CAGACCATCC TGATGCTCAT GACCTTCTTT GTCCTAATGT	960
CCATTTTCGA CAGCATTGTC TCCTGTTCAA GAACTATGTA TCTGAATGAT CCAACATCTT	1020
ACTATATTCA AATATTTGTA GTGGACATCT ATGCCACAGT CAGCCCTTTT GTGTTTATGA	1080
GCACTGGAAA ACATATAGTT AACTTTTTGA AGTCCATGTG TGTGAGGGTG AAGAATGTTT	1140
GAATATTCAT TAATGGACAA GATCCTTTAA GAGGAGCCAA TGTAGTCATC AGAACTGTCA	1200
GTCATGGTGT GCTGTCTATG TGCTTTGGTA AATGTGAATC ATGAAGTTGT TTTTCTGGTA	1260
AAATGATTTA CTTTAACCAA CTCATGATTG TAAACATGTA ACAGGAGATT AAACAATATC	1320
CCCTTCGGAA A	1331

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

0385476.070304

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AATTCGGCAC GAGCAAAGGC AGGGAAGATG CTCCACTGGG ATGTCATGTC TCTATGCTCC 60  
ACAGTGGAAG AGTTGTCACA TTGTACAAAC ACTAAAATTA CGAATTGCTC ACAGGCACTA 120  
AAAGCTTCCT TAATCCTGTG CAGGATCTCC TCAGGTACAG AGTCCTCCTG ATACGTCTAT 180  
CTGGTCAGAG GAAAGAGCTG ATCAGTCATT AACAGAGCTG ATTTGGTCCC TCCAAGGTCA 240  
CATGACAAGG ACTGTATGAG AAAACCAGCA GTGACATGTC TATAGAGATC ATTCTGTGCC 300  
ACACCCAGCT CCATGTTTGG TTTGTGGTAT TTGCTTCCTA TCCACATACA ATGAATAAAG 360  
ACAACACACT CCATGTTGAC ACAATCATGA AAATCACTAT GTTCTCTGAA GTGAGTGTTG 420  
GCATCTTAGC TAACAGTATC CTGTTTTTTG GTCACCTGTG CATGCTCCTT GGAGAGAACA 480  
AGCCTAAGCC CATTATCTC TACATTGCAT CCTTGTCCCT AACACAATA ATGCTGCTTA 540  
TAACTATGGG ACTCATAGCT GCTGACATGT TTATTTCTCA GGGGATATGG GATTCTACCT 600  
CATGCCAGTC CTTATCTAT TTGCACAGGC TTTCGAGGGG TTTTACCCTT AGTGCTGCCT 660  
GTCTGCTGAA TGTCTTTTGG ATGATCACTC TCAGTTCTAA AAAATCCTGT TTAACAAAGT 720  
TTAAACATAA CTCTCCCCAT CACATCTCAG GTGCCTTTCT TCTCCTCTGT GTTCTCTACA 780  
TGTGTTTTAG CAGTCACCTT ATTTTATCGA TTATTGCTAC CCCTAACTTG ACCTCAGATA 840  
ATTTTATGTA TGTTACTAAG TCCTGTTTAT TTCTACCCAT GTGTTACTCC AGAACAAGCA 900  
TGTTTTCCAC AACAATTGCT GTCAGGGAAG CCTTTTTTAT CGGTCTCATG GCCCTGTCCA 960  
GTGGGTACCT GGTGGCTTTC CTCTGGAGAC ACAGGAAGCA GGCCAGCAT CTTACAGCA 1020

090646 090646

(2) INFORMATION FOR SEQ ID NO:5:

(A) LENGTH: 1053 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TTTTTCCCA	CCTCTTCATG	CTCTTTGAAA	AGAACAGATC	TAAGCCCATT	GATCTCTACA	60
TTGCTTTCTT	ATCCTTAACC	CAACTAATGC	TGCTTATAAC	TATTGGACTT	ATAGCTGCAG	120
ACATGTTTAT	GTCTCGGGGG	AGATGGGATT	CTACCACATG	CCAGTCCCTT	ATCTATTTGG	180
ACAGGCTTTT	GAGGGGTTTT	ACCCTTTGTG	CTACCTGTCT	GCTGAATGTC	CTTTGGACCA	240
TCACTCTCAG	TCCTAGAAGC	TCCTGTTTAA	CAACATTTAA	ACATAAATCT	CCCCATCACA	300

TCTCAGGTGC CTTTCTTTTC TTCTGTGTTC TCTATATATC TTTTGGCAGT CACCTCTTTT 360  
TATCAACAAT TGCTACCCCC AATTTGACTT CAGATAATTT TATGTATGTT ACTAAATCCT 420  
GTTCAATTTCT ACCCATGAGT TACTCCAGAA CAAGCATGTT TTCCACACCA ATGGCCATCA 480  
GGGAAGCCCT TCTTATTGGT CTCATTGGCC TGTCCAGTGG GTACATGGTT GCTTTCCTAT 540  
GGAGACACAA GAATCAGGCC CGGCATCTTC ACAGCACCAG CCTTTCTTCA AAAGTGTCCC 600  
CAGAGCAAAG GGCCACCAGG ACCATCATGA TTCTCATGAG CTTCTTTGTG GTTCTCTACA 660  
TTTTGGAAAA TGTTGTCTTC TACTCTAGGA TGACATTCAA GGATGGGTCA ATGTTCTACT 720  
GTGTCCAAAT TATTGTGTCC CATAGCTATG CCACCATCAG CCCTTTTGTG TTTATTTGCA 780  
CAGAAAAGCG TATAATTAAA CTTTGGGGGT CAATGTCTAG CAGAATAGTA AGTATTTGAT 840  
TACTCAGTGA TGGATATGGT CCCTTAATAT AAACCAATAT GTTGTCTATA TAACTATGGA 900  
TCATGACATA TTGGGGACAT TCTGTGTCTT AAATTTATAA AAAAAATTTT CTTTTTTTGT 960  
GTTTAATCTG TTTCCCTTGT GTGTGGATGA TAAGTATATA AAGGGAAATT AAACAGCGTG 1020  
TCCCCTCAGA TATCCAAAAA AAAAAAAAAA AAA 1053

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3076 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

0969846-070304



GGGCTGCAGG AATTCGGCAC GAGTCAGAGT CCTTCCCTGC TATGTGTATC TGGAGCCAGC	60
GACTCTTCTA TGGAGAGCAG CTGTGCAGGC AGGTGGTGGG GCGGAAGAAG GCGTGCTGCT	120
GTGACATCAT CAAGATGCTG CCTAGCCCTG CGTCGCTGCT CTTCTGAGGA AGCAGGAGAC	180
TGACCCCTGT GACAATGACT TGATGAGTCA CTCTGTTGTC TACTTACCCT AGTTCTTTGT	240
CCCATACAAT GAGGAGAATC AGCACACTGT ATGGAGTTGT TGACAAGCAA GCTATATTTT	300
TCTCTGAAGT AGTCATCGGG ATCTCATTCA ACAGTATCCT CTTCCCTCTC CACATCTTTC	360
AGTTCCTTCT TGAGCGTAGG CTCCGGATCA CTGACCTGAT CATCAGTCTC TTGGCCCTCA	420
TCCACCTTGG GATGCTAACA GTCATGGGAT TCAGAGCTGT TGATATTTTT GCATCTCAGA	480
ATGTGTGGAA TGACATCAAA TGCAAATCCC TTGCCCCTT ACACAGACTT TTGAGGGGCC	540
TCTCTCTTTG TGCTACCTGT CTGCTGAGTA TCTTCCAGGC CATCACCTT AGCCCCAGAA	600
GCTCCTGTTT AGCAAAGTTC AAATATAAAT CCACACAGCA CAGCCTGTGT TCCCTTCTTG	660
TGCTCTGGGC CTTCTACATG TCCTGTGGTA CTCACTACTC CTTACCATC GTTGCTGACT	720
ACAACTTCTC TTCACGCAGT CTCATATTTG TCACTGAATC CTGCATTATT TTACCCATGG	780
ATTACATCAC CAGGGATTTA TTTTTCATAT TGGGGATATT TCGGGATGTG TCCTTCATAG	840
GTCTCATGGC CCTCTCCAGC GGGTACATGG TGGCCCTCTT GTGCAGACAC AGGAAACAGG	900
CCCAGCATCT TCACAGGACC AGCCTTTCTC CAAAAGCATC CCCAGAGCAA AGGGCCACCA	960
GGACCATCCT GTTGCTCATG AGCTTCTTTG TGTGATGTA CTGCTTGGAC TGCACCATAT	1020
CCGCCTCCAG ACTTATGCAC AACGGTGAAC CAATCCACCA CAGTATTCAG ATGATGGTCT	1080
CCAATAGCTA TGCCACCCTC AGCCCTTTCG TGTTAATTGT TACTGAAAAT CGAATTAGTA	1140
GGTTTTTGAA GTCCTTGCTA GGAAGGACAG TAGATGCTTA AGTATTGAGG GGAGGCAGGC	1200
CCACTAAAGG AGCCAATATG CTAGCTACTG AATAATGAAT CCTGGCCTAG TCCTCATGCA	1260

3344330

ATCCTGAACA AATTAATACA TGA CTCATGC TTCGT TAAAC CTGCTTCTTT TGAAATGTGT 1320  
ATTACCAACA CCTGTAGATA TTTGAGTCAA ATTTCTTCAT GTGTATTTCT TCTCAGTGTC 1380  
AGTAGGGGAC ATCTGTGACA CTTTCACAGA TTAGGGTAAC TTGTGCACTT ATCAATAAGC 1440  
TAAAGTGTAC AGCACATTTT ACTAAGCCAA TTATCTCAAC AGTTTGTTTT CTACCCAATT 1500  
AAATATGTAA ATGTTACCAC CAAAAAAAAA AAAAAAAAAA 1538

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TTGGGGTAAA ACGGCTCGAT GACTTCCACA TGTTTTGCCA TGGCAGAATC TGCTCCATGC 60  
GGGACAAGAA AATCTCTTTT CTGGTCTGAC GGGCTTACTG CTGAATTCAC TGTCGGCGAA 120  
GGTAAGTTGA TGA CTCATGA TGAACCCTGT TCTATGGCTC CAGATGACAA ACATGATCTC 180  
ATATCAGGGA CTTGTTGCA CCTTCCCTAA CAGTATCCTG TTTTTTGCCC ACCTCTGCAT 240  
GTTCTTTGAA GAGAACAGGT CTAAGCCCAT TGATCTGTGC ATTGCTTTCT TATCCTTAAC 300  
CCA ACTAATG CTGCTTGTA CTATGGGACT CATAGCTGCA GACATGTTA TGGCTCAGGG 360  
GATATGGGAT ATTACCACAT GCAGGTCCCT TATCTATTTT CACAGACTTT TGAGGGGTTT 420  
CAACCTTTGT GCTGCCTGTC TACTGCATAT CCTTTGGACC TTCACTCTCA GTCCTAGAAG 480

(2) INFORMATION FOR SEQ ID NO:8:

(A) LENGTH: 315 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Met	Asn	Lys	Asn	Ser	Arg	Leu	Tyr	Thr	Asp	Ser	Asn	Ile	Arg	Asn	
1				5					10					15		
Thr	Phe	Phe	Ala	Glu	Ile	Gly	Ile	Gly	Val	Ser	Ala	Asn	Ser	Leu	Leu	
			20					25						30		
Leu	Leu	Phe	Asn	Ile	Phe	Lys	Leu	Ile	Cys	Gly	Gln	Arg	Ser	Arg	Leu	
			35				40						45			
Thr	Asp	Leu	Pro	Ile	Gly	Leu	Leu	Ser	Leu	Ile	Asn	Leu	Leu	Met	Leu	
			50				55					60				
Leu	Met	Thr	Ala	Phe	Ile	Ala	Thr	Asp	Thr	Phe	Ile	Ser	Trp	Arg	Gly	
			65			70					75				80	
Trp	Asp	Asp	Ile	Ile	Cys	Lys	Ser	Leu	Leu	Tyr	Leu	Tyr	Arg	Thr	Phe	
			85						90					95		
Arg	Gly	Leu	Ser	Leu	Cys	Thr	Ser	Cys	Leu	Leu	Ser	Val	Leu	Gln	Ala	
			100					105						110		
Ile	Ile	Leu	Ser	Pro	Arg	Ser	Ser	Cys	Leu	Ala	Lys	Phe	Lys	His	Lys	
			115					120						125		
Pro	Ser	His	His	Ile	Ser	Cys	Ala	Ile	Leu	Ser	Leu	Ser	Val	Leu	Tyr	
			130				135					140				
Met	Phe	Ile	Ser	Ser	His	Leu	Leu	Val	Ser	Ile	Ile	Ala	Thr	Pro	Asn	
			145			150				155					160	
Leu	Thr	Thr	Asn	Asp	Phe	Ile	His	Val	Thr	Gln	Trp	Cys	Ser	Ile	Leu	
			165						170					175		
Pro	Met	Ser	Tyr	Leu	Met	Gln	Ser	Met	Phe	Ser	Thr	Leu	Leu	Ala	Ile	
			180					185						190		
Arg	Asp	Val	Phe	Leu	Ile	Ser	Leu	Met	Val	Leu	Ser	Thr	Trp	Tyr	Met	
			195				200						205			

0903416 0903416

Val Ala Leu Leu Cys Arg His Arg Lys Gln Thr Arg His Leu Gln Gly  
 210 215 220

Thr Ser Leu Ser Pro Lys Ala Ser Pro Glu Gln Arg Ala Thr Arg Ser  
 225 230 235 240

Ile Leu Met Leu Met Ser Leu Phe Val Leu Met Ser Val Phe Asp Ser  
 245 250 255

Ile Val Cys Ser Ser Arg Thr Met Tyr Leu Asn Asp Pro Ile Ser Tyr  
 260 265 270

Ser Tyr Gln Leu Phe Met Val His Ile Tyr Ala Thr Val Ser Pro Phe  
 275 280 285

Val Phe Ile Val Thr Glu Lys His Ile Val Asn Ser Leu Arg Ser Met  
 290 295 300

Cys Val Lys Val His Glu Cys Leu Asn Ile Pro  
 305 310 315

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Met Asn Lys Asn Ser Arg Leu His Ile Asp Ser Asn Ile Arg Asn  
 1 5 10 15

Thr Phe Phe Thr Glu Ile Gly Ile Gly Val Ser Ala Asn Ser Leu Leu  
 20 25 30

096964-073904

Leu	Leu	Phe	Asn	Ile	Phe	Lys	Phe	Ile	His	Gly	Gln	Arg	Ser	Arg	Leu
	35						40					45			
Thr	Asp	Leu	Pro	Ile	Gly	Leu	Leu	Ser	Leu	Ile	Asn	Leu	Leu	Met	Leu
	50					55					60				
Leu	Ile	Met	Ala	Cys	Ile	Ala	Thr	Asp	Ile	Phe	Ile	Ser	Cys	Arg	Arg
65				70						75					80
Trp	Asp	Asp	Ile	Ile	Cys	Lys	Ser	Leu	Leu	Tyr	Leu	Tyr	Arg	Thr	Phe
			85						90					95	
Arg	Gly	Leu	Ser	Leu	Ser	Thr	Thr	Cys	Leu	Leu	Ser	Val	Leu	Gln	Ala
		100						105					110		
Ile	Ile	Leu	Ser	Pro	Arg	Ser	Ser	Cys	Leu	Ala	Lys	Tyr	Lys	His	Lys
	115						120					125			
Pro	Pro	His	His	Ile	Phe	Cys	Ala	Met	Leu	Phe	Leu	Ser	Val	Leu	Tyr
	130					135					140				
Met	Phe	Ile	Ser	Ser	His	Leu	Leu	Leu	Ser	Ile	Ile	Ala	Thr	Pro	Asn
145					150					155					160
Leu	Thr	Thr	Asn	Asp	Phe	Ile	His	Val	Ser	Gln	Ser	Cys	Ser	Ile	Leu
			165						170					175	
Pro	Met	Ser	Tyr	Leu	Met	Gln	Ser	Met	Phe	Ser	Thr	Leu	Leu	Ala	Ile
		180						185						190	
Arg	Asn	Val	Phe	Leu	Ile	Ser	Leu	Ile	Val	Leu	Ser	Thr	Trp	Tyr	Met
		195					200					205			
Val	Ala	Leu	Leu	Cys	Arg	His	Arg	Lys	Gln	Thr	Arg	His	Leu	Gln	Asp
	210					215					220				
Thr	Ser	Leu	Ser	Arg	Lys	Ala	Ser	Pro	Glu	Gln	Arg	Ala	Thr	Arg	Ser
225					230					235					240
Ile	Leu	Met	Leu	Arg	Ser	Leu	Phe	Gly	Leu	Met	Ser	Ile	Phe	Asp	Ser
			245						250					255	

Leu Met Gly Ala Phe Ile Ala Ile Asp Ile Phe Ile Ser Trp Arg Gly  
65 70 75 80

Trp	Asp	Asp	Ile	Ile	Cys	Lys	Phe	Leu	Val	Tyr	Leu	Tyr	Arg	Ser	Phe	85	90	95
Arg	Gly	Leu	Ser	Leu	Cys	Thr	Thr	Cys	Met	Leu	Ser	Val	Leu	Gln	Ala	100	105	110
Ile	Thr	Leu	Ser	Pro	Arg	Ser	Ser	Cys	Leu	Ala	Lys	Phe	Lys	His	Lys	115	120	125
Ser	Pro	His	His	Val	Ser	Cys	Ala	Ile	Ile	Ser	Leu	Ser	Ile	Leu	Tyr	130	135	140
Met	Phe	Ile	Ser	Ser	His	Leu	Leu	Val	Ser	Ile	Asn	Ala	Thr	Pro	Asn	145	150	155
Leu	Thr	Thr	Asn	Asn	Phe	Met	Gln	Val	Thr	Gln	Ser	Cys	Tyr	Ile	Ile	165	170	175
Pro	Leu	Ser	Tyr	Leu	Met	Gln	Ser	Met	Phe	Ser	Thr	Leu	Leu	Ala	Ile	180	185	190
Arg	Asp	Ile	Ser	Leu	Ile	Ser	Leu	Met	Val	Leu	Ser	Thr	Cys	Tyr	Met	195	200	205
Glu	Val	Leu	Leu	Cys	Arg	His	Arg	Asn	Gln	Ile	Gln	His	Leu	Gln	Gly	210	215	220
Thr	Asn	Leu	Ser	Pro	Lys	Ala	Ser	Pro	Glu	Gln	Arg	Ala	Thr	Gln	Thr	225	230	235
Ile	Leu	Met	Leu	Met	Thr	Phe	Phe	Val	Leu	Met	Ser	Ile	Phe	Asp	Ser	245	250	255
Ile	Val	Ser	Cys	Ser	Arg	Thr	Met	Tyr	Leu	Asn	Asp	Pro	Thr	Ser	Tyr	260	265	270
Tyr	Ile	Gln	Ile	Phe	Gly	Val	Asp	Ile	Tyr	Ala	Thr	Val	Ser	Pro	Phe	275	280	285
Val	Phe	Met	Ser	Thr	Glu	Lys	His	Ile	Val	Asn	Phe	Leu	Lys	Ser	Met	290	295	300



Cys Val Arg Val Lys Asn Val  
305 310

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Asn Lys Asp Asn Thr Leu His Val Asp Thr Ile Met Lys Ile Thr  
1 5 10 15

Met Phe Ser Glu Val Ser Val Gly Ile Leu Ala Asn Ser Ile Leu Phe  
20 25 30

Phe Gly His Leu Cys Met Leu Leu Gly Glu Asn Lys Pro Lys Pro Ile  
35 40 45

His Leu Tyr Ile Ala Ser Leu Ser Leu Thr Gln Leu Met Leu Leu Ile  
50 55 60

Thr Met Gly Leu Ile Ala Ala Asp Met Phe Ile Ser Gln Gly Ile Trp  
65                      70                      75                      80

Asp Ser Thr Ser Cys Gln Ser Leu Ile Tyr Leu His Arg Leu Ser Arg  
85 90 95

Gly Phe Thr Leu Ser Ala Ala Cys Leu Leu Asn Val Phe Trp Met Ile  
100 105 110

Thr Leu Ser Ser Lys Lys Ser Cys Leu Thr Lys Phe Lys His Asn Ser  
115 120 125

(2) INFORMATION FOR SEQ ID NO:12:

(A) LENGTH: 278 amino acids  
(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Phe Ser His Leu Phe Met Leu Phe Glu Lys Asn Arg Ser Lys Pro Ile  
1 5 10 15  
Asp Leu Tyr Ile Ala Phe Leu Ser Leu Thr Gln Leu Met Leu Leu Ile  
20 25 30  
Thr Ile Gly Leu Ile Ala Ala Asp Met Phe Met Ser Arg Gly Arg Trp  
35 40 45  
Asp Ser Thr Thr Cys Gln Ser Leu Ile Tyr Leu Asp Arg Leu Leu Arg  
50 55 60  
Gly Phe Thr Leu Cys Ala Thr Cys Leu Leu Asn Val Leu Trp Thr Ile  
65 70 75 80  
Thr Leu Ser Pro Arg Ser Ser Cys Leu Thr Thr Phe Lys His Lys Ser  
85 90 95  
Pro His His Ile Ser Gly Ala Phe Leu Phe Phe Cys Val Leu Tyr Ile  
100 105 110  
Ser Phe Gly Ser His Leu Phe Leu Ser Thr Ile Ala Thr Pro Asn Leu  
115 120 125  
Thr Ser Asp Asn Phe Met Tyr Val Thr Lys Ser Cys Ser Phe Leu Pro  
130 135 140  
Met Ser Tyr Ser Arg Thr Ser Met Phe Ser Thr Pro Met Ala Ile Arg  
145 150 155 160  
Glu Ala Leu Leu Ile Gly Leu Ile Gly Leu Ser Ser Gly Tyr Met Val

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T02020" 9TH35860

170

Met Arg Arg Ile Ser Thr Leu Tyr Gly Val Val Asp Lys Gln Ala Ile  
1 5 10 15

Phe	Phe	Ser	Glu	Val	Val	Ile	Gly	Ile	Ser	Phe	Asn	Ser	Ile	Leu	Phe	
20			25						30							
Leu	Phe	His	Ile	Phe	Gln	Phe	Leu	Leu	Glu	Arg	Arg	Leu	Arg	Ile	Thr	
35			40						45							
Asp	Leu	Ile	Ile	Ser	Leu	Leu	Ala	Leu	Ile	His	Leu	Gly	Met	Leu	Thr	
50			55						60							
Val	Met	Gly	Phe	Arg	Ala	Val	Asp	Ile	Phe	Ala	Ser	Gln	Asn	Val	Trp	
65			70						75						80	
Asn	Asp	Ile	Lys	Cys	Lys	Ser	Leu	Ala	His	Leu	His	Arg	Leu	Leu	Arg	
85				90						95						
Gly	Leu	Ser	Leu	Cys	Ala	Thr	Cys	Leu	Leu	Ser	Ile	Phe	Gln	Ala	Ile	
100			105						110							
Thr	Leu	Ser	Pro	Arg	Ser	Ser	Cys	Leu	Ala	Lys	Phe	Lys	Tyr	Lys	Ser	
115			120						125							
Thr	Gln	His	Ser	Leu	Cys	Ser	Leu	Leu	Val	Leu	Trp	Ala	Phe	Tyr	Met	
130			135						140							
Ser	Cys	Gly	Thr	His	Tyr	Ser	Phe	Thr	Ile	Val	Ala	Asp	Tyr	Asn	Phe	
145			150						155						160	
Ser	Ser	Arg	Ser	Leu	Ile	Phe	Val	Thr	Glu	Ser	Cys	Ile	Ile	Leu	Pro	
165				170						175						
Met	Asp	Tyr	Ile	Thr	Arg	His	Leu	Phe	Phe	Ile	Leu	Gly	Ile	Phe	Arg	
180			185						190							
Asp	Val	Ser	Phe	Ile	Gly	Leu	Met	Ala	Leu	Ser	Ser	Gly	Tyr	Met	Val	
195			200						205							
Ala	Leu	Leu	Cys	Arg	His	Arg	Lys	Gln	Ala	Gln	His	Leu	His	Arg	Thr	
210			215						220							
Ser	Leu	Ser	Pro	Lys	Ala	Ser	Pro	Glu	Gln	Arg	Ala	Thr	Arg	Thr	Ile	
225			230						235						240	

Gly Arg Thr Val Asp Ala  
305 310

(A) LENGTH: 307 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ile Ala Phe Leu Ser Leu Thr Gln Leu Met Leu Leu Val Thr Met Gly  
50 55 60

Leu Ile Ala Ala Asp Met Phe Met Ala Gln Gly Ile Trp Asp Ile Thr  
65 70 75 80

Thr Cys Arg Ser Leu Ile Tyr Phe His Arg Leu Leu Arg Gly Phe Asn  
85 90 95

Leu Cys Ala Ala Cys Leu Leu His Ile Leu Trp Thr Phe Thr Leu Ser  
100 105 110

Pro Arg Ser Ser Cys Leu Thr Lys Phe Lys His Lys Ser Pro His His  
115 120 125

Ile Ser Gly Ala Tyr Leu Phe Phe Cys Val Leu Tyr Met Ser Phe Ser  
130 135 140

Ser His Leu Phe Val Leu Val Ile Ala Thr Ser Asn Leu Thr Ser Asp  
145 150 155 160

His Phe Met Tyr Val Thr Gln Ser Cys Ser Leu Leu Pro Met Ser Tyr  
165 170 175

Ser Arg Thr Ser Thr Phe Ser Leu Leu Met Val Thr Arg Glu Val Phe  
180 185 190

Leu Ile Ser Leu Met Ala Leu Ser Ser Gly Tyr Met Val Thr Leu Leu  
195 200 205

Trp Arg His Lys Lys Gln Ala Gln His Leu His Ser Thr Arg Leu Ser  
210 215 220

Ser Lys Ala Ser Pro Gln Gln Arg Ala Thr Arg Thr Ile Leu Leu Leu  
225 230 235 240

Met Thr Phe Phe Val Val Phe Tyr Ile Leu Gly Thr Val Ile Phe His  
245 250 255

Ser Arg Thr Lys Phe Lys Asp Gly Ser Ile Phe Tyr Cys Val Gln Ile  
260 265 270

Ile Val Ser His Ser Tyr Ala Thr Ile Ser Pro Phe Val Phe Val Phe  
275 280 285

0909416 070304

Val Asn Thr  
305

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Thr Ile Phe Thr Leu Met Thr Phe Gln Asp Val Ser Leu Gln Leu Met  
100 105 110



Leu Val Ala Ser Ala Met Ala  
65 70

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: peptide

Gly Gln Arg Ser Arg Leu Thr Asp Leu Pro Ile Gly Leu Leu Ser Leu  
1 5 10 15

Ile Asn Leu Leu Met Leu Leu Ile Met Ala Cys Ile Ala Thr Asp Ile  
20 25 30

Phe Ile Ser Cys Arg Arg Trp Asp Asp Ile Ile Cys Lys Ser Leu Leu  
35 40 45

Tyr Leu Tyr Arg Thr Phe Arg Gly Leu Ser Leu Ser Thr Thr Cys Leu  
50 55 60

Leu Ser Val Leu Gln Ala Ile Ile Leu Ser  
65 70

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Lys Cys Lys Ser Leu Ala His Leu His Arg Leu Leu Arg Gly Leu Ser  
1 5 10 15  
Leu Cys Ala Thr Cys Leu Leu Ser Ile Phe Gln Ala Ile Thr Leu Ser  
20 25 30  
Pro Arg Ser Ser Cys Leu Ala Lys Ser Thr Gln His Ser Leu Cys Ser  
35 40 45  
Leu Leu Val Leu Trp Ala Phe Tyr Met Ser Cys Gly Thr His Tyr Ser  
50 55 60  
Phe Thr Ile Val Ala Asp Tyr Asn Phe Ser Ser Arg Ser Leu Ile Phe  
65 70 75 80  
Val Thr Glu Ser Cys Ile Ile Leu Pro Met Asp Tyr Ile Thr Arg Asp  
85 90 95  
Leu Phe Phe Ile Leu Gly Ile Phe Arg Asp Val Ser Phe Ile Gly Leu  
100 105 110  
Met Ala Leu Ser Ser Gly Tyr Met Val Ala Leu Leu Cys Arg His Arg  
115 120 125  
Lys Gly Ala Gln His Leu His Arg Thr Ser Leu Ser Pro Lys Ala Ser  
130 135 140  
Pro Glu Gln Arg Ala Thr Arg Thr Ile Leu Leu Leu Met Ser Phe Phe  
145 150 155 160  
Val Leu Met Tyr Cys Leu Asp Cys Thr Ile Ser Ala Ser Arg  
165 170

090946 07301